

M D F G L A L L L A G L L G O S L O V K P L O GGTGGAGCCCCGGAGCCGGTGGCCGTGGCCTTGGGCGCCTCGCGCCAGCTCACCTGCCGCCTGGCCTGCCCTGCCGACC 160 V E P P E P V V A V A L G A S R Q L T C R L A C A D R G A S V O W R G L D T S L G A V O S D T G R S V L T GTGCGCAACGCCTCGCTGTCGGCGGCCGGGACCCGCGTGTGCGTGGGCTCCTGCGGGGGCCGCACCTTCCAGCACACCGT 320 V R N A S L S A A G T R V C V G S C G G R T F O H T V GCAGCTCCTTGTGTACGCCTTCCCGGACCAGCTGACCGTCTCCCCAGCAGCCCTGGTGCCTGGTGACCCGGAGGTGGCCT 400 O L L Y Y A F P D Q L T V S P A A L V P G D P E V A GTACGGCCCACAAAGTCACGCCCGTGGACCCCAACGCGCTCTCCTTCTCCCTGCTCGTCGGGGGCCAGGAACTGGAGGGG 480 C T A H K V T P V D P N A L S F S L L V G G Q E L E G GCGCAAGCCCTGGGCCCGGAGGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGACGTGCTGTTCAGGGTGACAGA 560 A O A L G P E V O E E E E P O G D E D V L F R V T E R W R L P P L G T P V P P A L Y C O A T M R L P G L AGETEAGGEAGGEAGGECATCCCCGTCCTGCAGAGCCCGACCTCCCGGAGCTCCCGGACACCACCTCCCGGAGCCT 720 ELSHROAIPVLH|SPTSPEPPDTTSPEP COMMOMOCACCTCCCGGGAGTCTCCCGACACCTCCCGGGGGTCTCCCGGACACCTCCCCAGGAGACCTCCCGACAC PNTTSPESPDTTSPESPDTTSQEPPDT CACCTCCCAGSASCCTCCCGACACCACCTCCCAGGAGCCTCCCGACACCACCTCCCGGAGCCTCCCGACAAGACCTCCC 880 T S C E P P D T T S O E P P D T T S P E P P D K T S OGGAGOCO GOCCOCCAGGAGGGCTCCACACACACCCCCAGGAGCCCAGGCTCCACCAGGACTEGCCGCCCTGAGATCTCC 960 PEPAPOOGSTHTPRSPGSTRTRRPEIS CASSCTGSSCCCASSCAGGGAGGAGGTGATCCCAACAGGCTCGTCCAAACCTGCGGGTGACCAGCTGCCCGGGGCTCTGTG 1040 $\texttt{C} \ \ \, \texttt{A} \ \ \, \texttt{G} \ \ \, \texttt{F} \ \ \, \texttt{T} \ \ \, \texttt{O} \ \ \, \texttt{G} \ \ \, \texttt{E} \ \ \, \texttt{V} \ \ \, \texttt{I} \ \ \, \texttt{P} \ \ \, \texttt{A} \ \ \, \texttt{G} \ \ \, \texttt{D} \ \ \, \texttt{O} \ \ \, \texttt{L} \ \ \, \texttt{P} \ \ \, \texttt{A} \ \ \, \texttt{L} \ \ \, \texttt{W}$ GASCASCASTSCSSTGCTGGGGACTGCTGCTCCTGGCCTGCCCACGTATCACCTCTGGAAACGCTGCCGGCACCTGGCTG 1120 S S & V L G L L L A L P T Y H L W K R C R H L A AGGACGACCACCACCACCACCTCTCTGAGGCTTCTGCCCCAGGTGTCGGCCTGGGCTGGGTTAAGGGGGACCGGCCAG 1200 EDDTHPPASLRLLPOVSAWAGLRGTGO GTCGGGATCASCCCTCCTGAGTGGCCAGCCTTTCCCCCTGTGAAAGCAAAATAGCTTGGACCCCTTCAAGTTGAGAACT 1280 V G I S P S CAASSIGIGSSIGASCACCOIGGGCCCCIGICGICAGGACCICCIGAGGCIIIGGCAAAIAAACCICCIAAAAIGAIAA 1600 AAAAAAAAAAAAAAAAA 1624

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PDTTSPESPDTTSQEPPDTTSPEPPDK
GACCTCCCCGGAGCCCGCCCCAGCAGGGCTCCACACCACCACCAGGAGCCCAGGGCTCCACCAGGACTCGCCGCCCTG 880 T S P E P A P Q Q S T H T P R S P G S T R T R R P
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CCGGCCAGGTCGGGATCAGCCCCTCCTGAGTGGCCAGCCTTTCCCCCCTGTGAAAGCAAAATAGCTTGGACCCCTTCAAGT 1200 T G O V G I S P S
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FIGURE 2

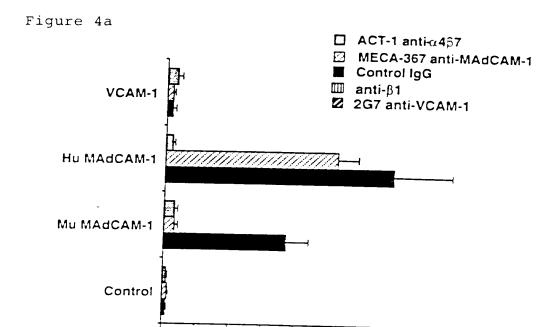
PCT/US96/02153

3/20 Figure 3

M D R G L A L L A <u>G</u> L L C L L <u>O P G C</u> G O S L Q Y GAAGCCCCTGCAGGTGGAGCCCCGGGAGCCGGTGGTGGCCGTGGCCGTGGGCGCCTCTCGCCAGCTCACCTGCCCCCTGG 180 K P L O V E P P F P V V A V A L G A S R O L 1 C R L DIADRIATIVO W RGLD TSLIAVOSDAGR AGCGTCCTCACCGTGCGCAACGCCTCGCTGTCGGCGGGGGCCGGGGACCCGTGTGTGCGTGGGCTCCTTGCGGGGGCCGCACCT1 320 S V L T V R N A S L S A A G T R V C Y G S C G G R T F CCAGCACACCGTGCGGCTCCTTGTGTACGCCTTCCCGSACCACCTCACCATCTCCCCGGCAGCCCTGGTGCCTGGTGACC 400 O H T Y R L L Y Y A F P O O L T I S P A A L Y P G D CGGAGGTGGCC1GTACGGCCAAAAAGTCACGCCTGTGGACCCCAATGCGCTCTCCTTCTCCTGCTGCTGCGGGGACCAC 480 LE VACTANK V TP V D P N A L S F S L I. L G D O C L C C A O A L G P E V E F C C C C C D O È E E D V L F CARGREDACAGAGGGCTGGCGGGCTGCCCACCCTGGGCAGCCTGTCCTGGCCGGGCTGTACTGCCAGGCCACGATGAGGG 640 RVTERWRLPTLATPVIPALYCOATMR L C G L E L S H R D A I P V L II G P T S R E P P D T T TECCOGSAACCCGGGGCGGGGACCTCCCCGGAGACCACCCCCCAGGAGGGGCCCAGGAGACCAGGAGCCCGGGCTC 800 S P E P R A A T S P E T T P Q C G S T H S P R S P G S TACCAGGACTTGCCGCCCTGAGATCTCCC43GC1GGGUUCACGGAGAGAGAGATCACAACAGGCTCGTCCAACACCTA TRICRPEIS DAGPIDGEVIPIGS SKP T G D C L P A A L W T S S A V L C L L L A I P T Y H CTCTGSAAAGGTTGCCGGCACCTGGCTGAGGAGCGGCGCCCACCGAGCTTCTCTGAGTAGCCAGGCTTCCCCCTGTR 1040 LWKRCRHLAEDGAHPFASLSSCPFPL. ANDGGAAAATAGGTTGGACCCCTTCAAGCTGAGAAC136°CCGGGCAAACCTGCCTGCCATTCTATTCAAACTCATCCC1 1120 CTOGTCACAGAGAGGGGACATTCTCATTGCCTCCTTTGG/AAGGCTCATCAGAAAAGAAGGGGACATCGTTTG 1200 TOCCOCCT ACCCGTGACCTGGAACCACCCCGCCCCCCGAGTCACCCCTGACTTTCTCACCGGAACCGAACGTACCTTCTTA 1280 CATATATTGATTCATGTGTCATATCTCCCTAAAATGTGTAAAACCACCTGTGCCCCGACCATGTGTGGCCCCTGCCATCA 1350 TGTANTCCCAGCACTTTRGGAGGCCGAGGTGGGTGGGTGGGTGGGTGGGTGGGGAGATGGAGACCATCCTGGCTAACCCGTGAA 1520 AGGCAGGAGAATGGGGTGAACCCGGGAGGCGGAGGTTGCAGTTGAGTTGAGATCCGGGCCACTGCACTTCAGCC1CGGGGAC 1680

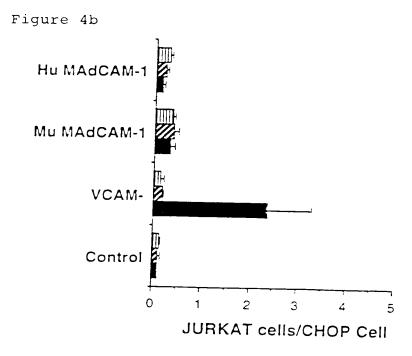
5





2

RPMI 8866 cells/CHOP Cell



1

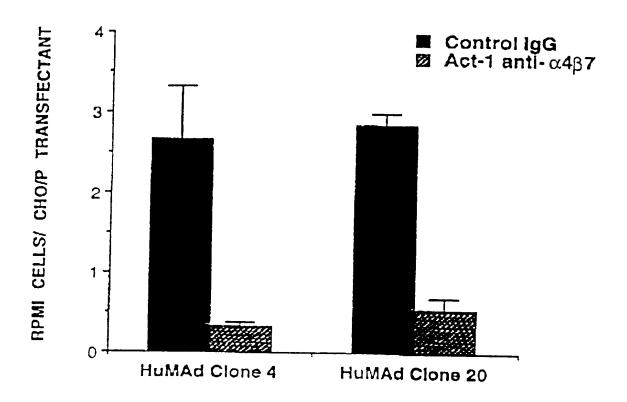
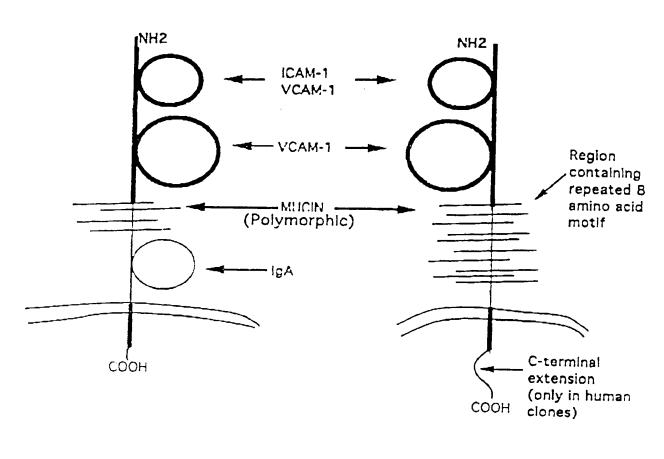


FIGURE 5

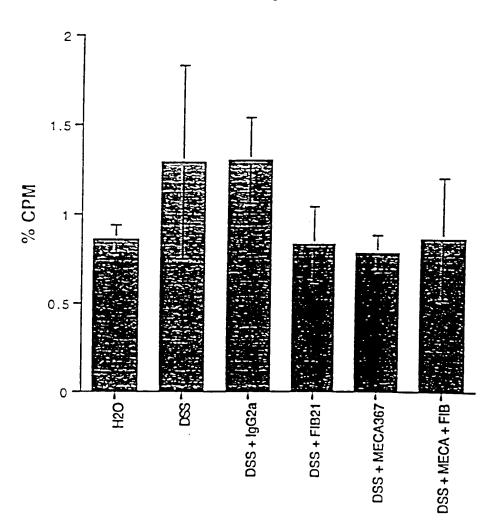


Murine MAdCAM-1 Human human clones MAdCAM-1

Figure 6

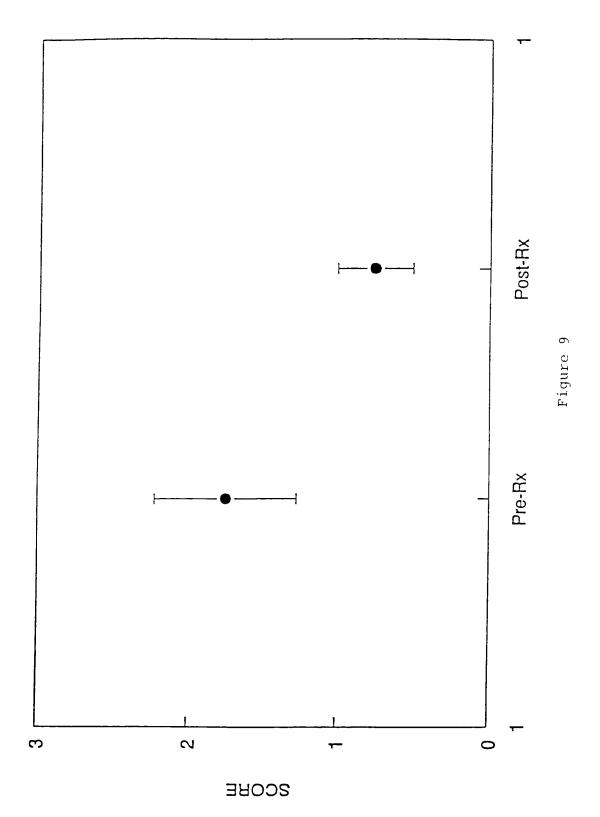
PCT/US96/02153 7/20 Rat IgG2a FIB-30 F1B-21 Ø :0: STRUCTURAL DAMAGE ASCENDING COLON FIGURE 7B TISSUE DESCENDING 2.5 0.5-.5-**EYCOS** Rat IgG2a F1B-30 F1B-21 至 ASCENDING COLON INFLAMMATION TISSUE FIGURE 7A DESCENDING COLON 2.5-0.5-1.5-**3003E**

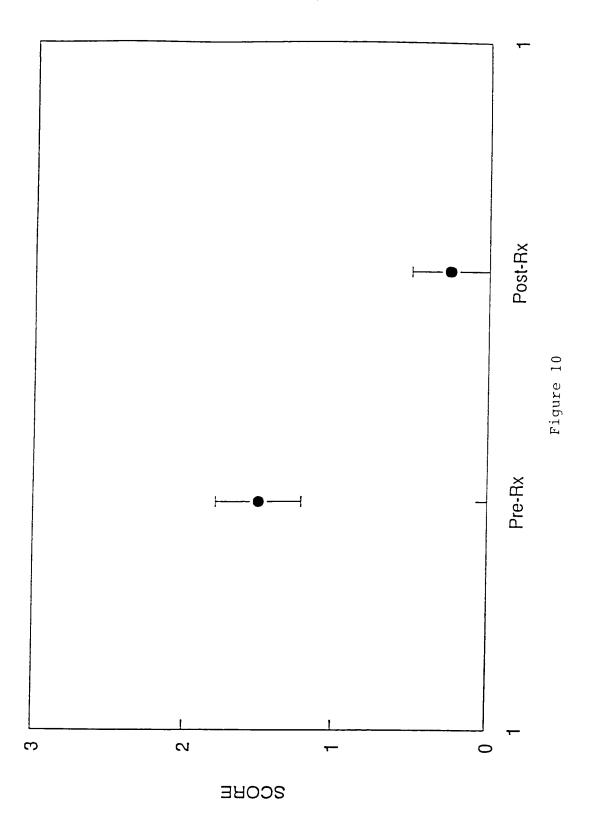
Figure 8



TREATMENT







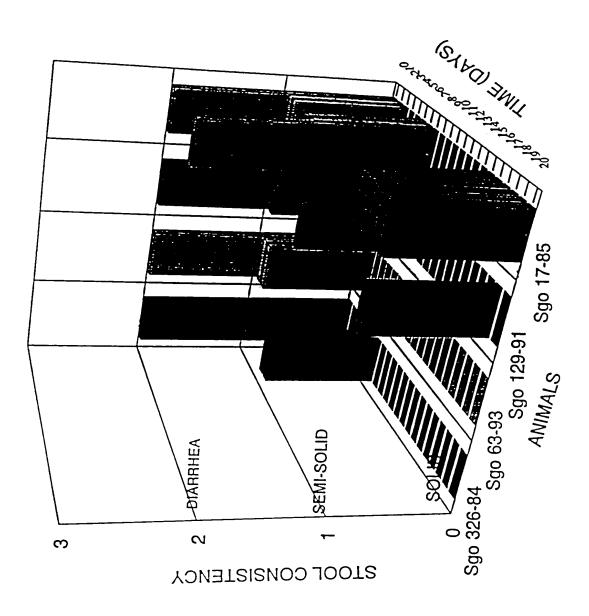
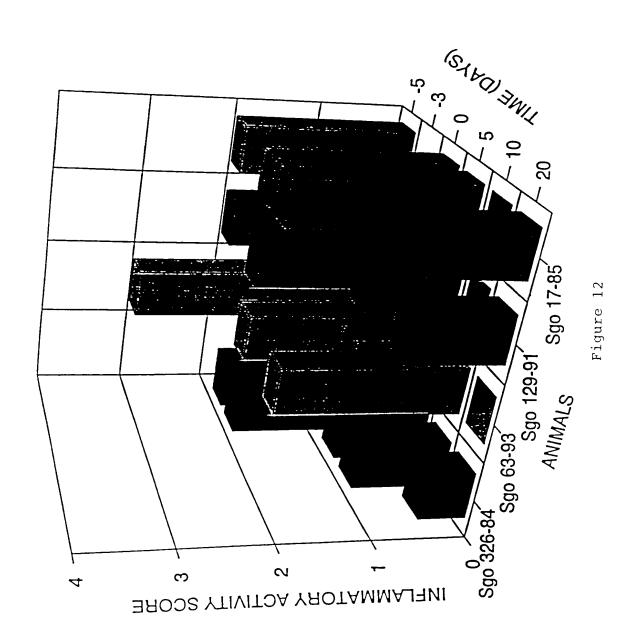
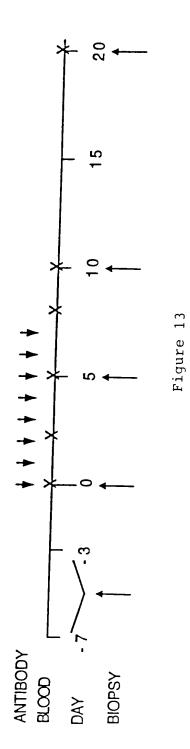


Figure 11





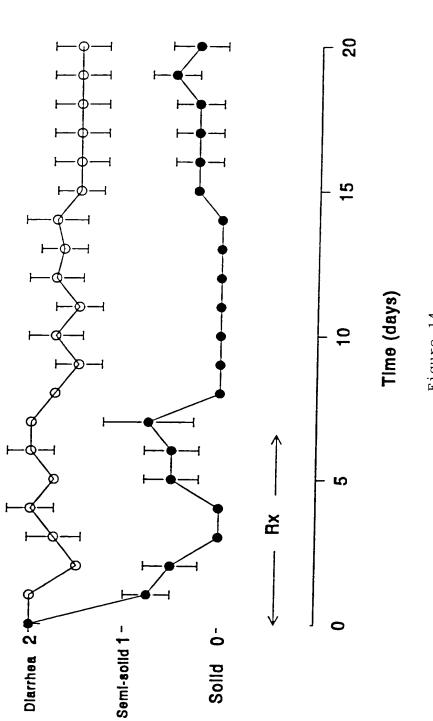
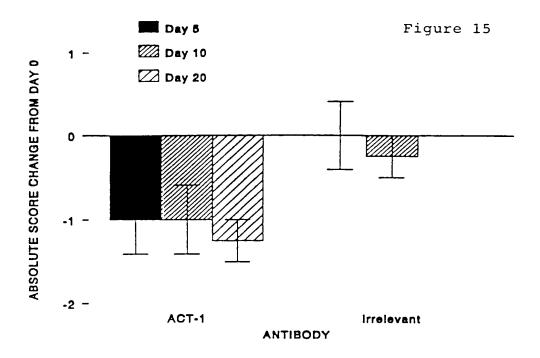
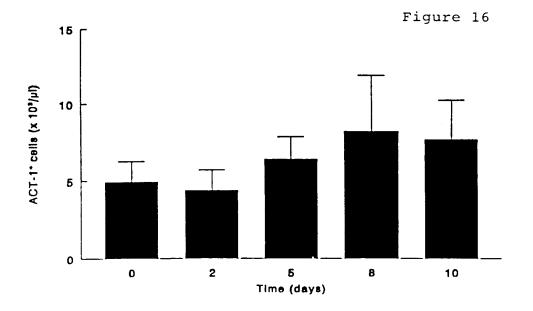
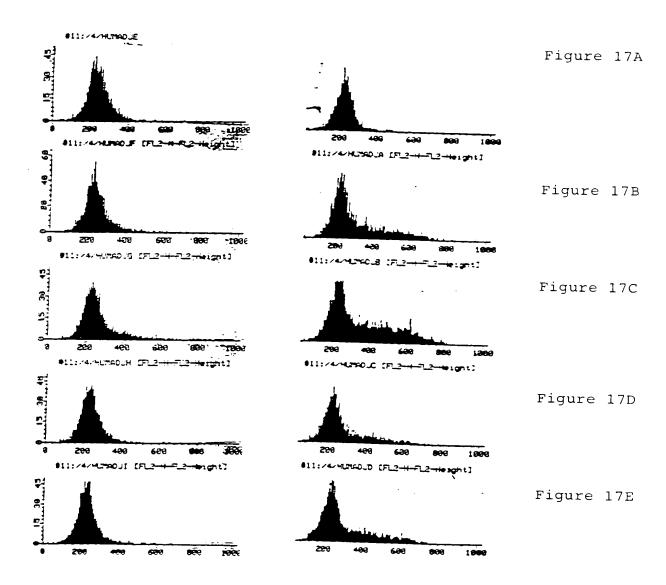


Figure 14







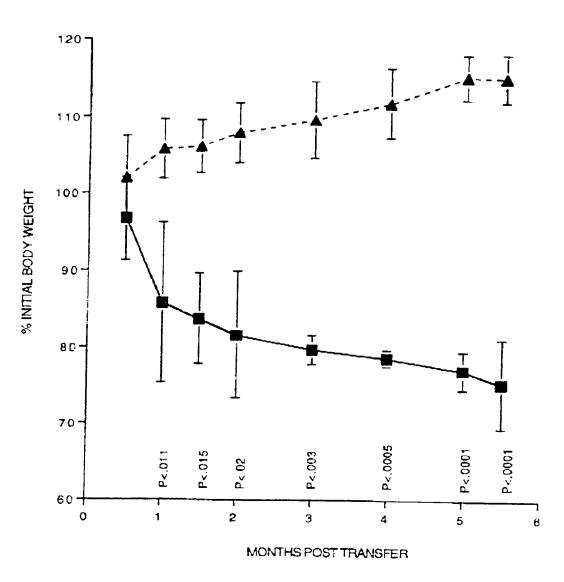


Figure 18

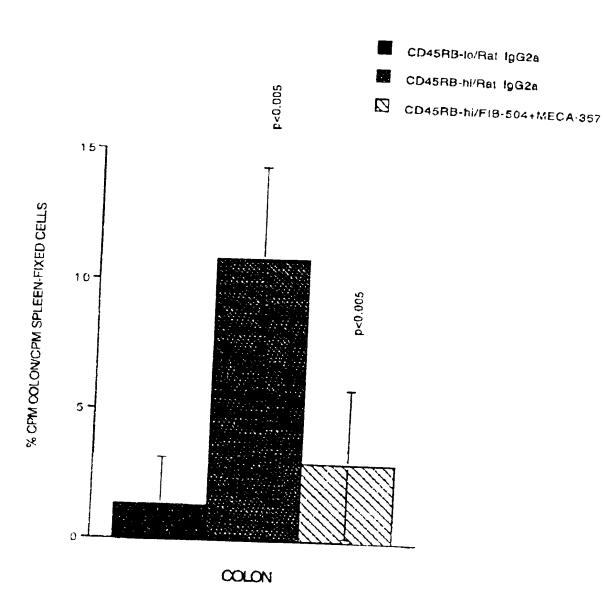


Figure 19

Figure 20

CD45RBlo/Rat 1gG2a

CD45RBhi/Rat IgG2a

E CD45RBhi/F1B-504

CD45RBhi/MECA-367

CD45RBhi/FIB504+MECA367

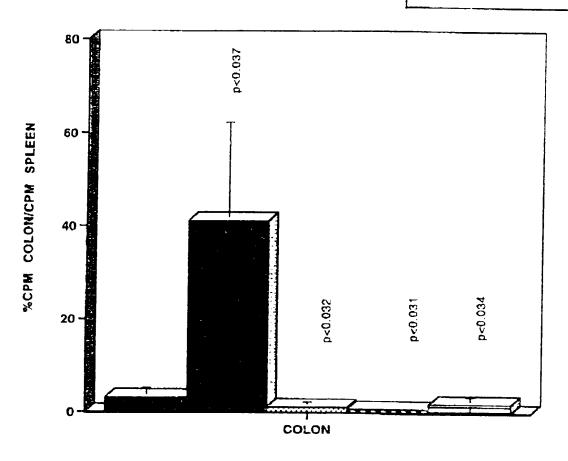




Figure 21 5007 400-300 **COUNT/APPEA** 200 100-

RIGHT COLON

LEFT COLON

Rat IgG2a

FIB504 + MECA387